

RAW SEQUENCE LISTING . DATE: 03/22/2001
PATENT APPLICATION: US/09/747,804 TIME: 11:46:44

Input Set : A:\09747804.txt
Output Set: N:\CRF3\03222001\I747804.raw

ENTERED

RAW SEQUENCE LISTING

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```

62          200          205          210
63 Pro Cys Ser His Ala Leu Pro Gln Gly Leu Ser Pro Gly Gln Val
64          215          220          225
65 Ile Ile Val Arg Gly Leu Val Leu Gln Glu Pro Lys His Phe Thr
66          230          235          240
67 Val Ser Leu Arg Asp Gln Ala Ala His Ala Pro Val Thr Leu Arg
68          245          250          255
69 Ala Ser Phe Ala Asp Arg Thr Leu Ala Trp Ile Ser Arg Trp Gly
70          260          265          270
71 Gln Lys Lys Leu Ile Ser Ala Pro Phe Leu Phe Tyr Pro Gln Arg
72          275          280          285
73 Phe Phe Glu Val Leu Leu Leu Phe Gln Glu Gly Gly Leu Lys Leu
74          290          295          300
75 Ala Leu Asn Gly Gln Gly Leu Gly Ala Thr Ser Met Asn Gln Gln
76          305          310          315
77 Ala Leu Glu Gln Leu Arg Glu Leu Arg Ile Ser Gly Ser Val Gln
78          320          325          330
79 Leu Tyr Cys Val His Ser
80          335
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 708
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
W--> 90 <220> FEATURE: -
91 <223> OTHER INFORMATION: 2687731
93 <400> SEQUENCE: 2
94 Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala
95 1 5 10 15
96 Ile Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro
97 20 25 30
98 Arg Leu Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser
99 35 40 45
100 Ile Tyr Met Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu
101 50 55 60
102 Leu Thr Phe Pro Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu
103 65 70 75
104 Leu Gln Thr Asn Asn Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe
105 80 85 90
106 Pro Val Asn Leu Thr Gly Leu Asp Leu Ser Gln Asn Asn Leu Ser
107 95 100 105
108 Ser Val Thr Asn Ile Asn Val Lys Lys Met Pro Gln Leu Leu Ser
109 110 115 120
110 Val Tyr Leu Glu Glu Asn Lys Leu Thr Glu Leu Pro Glu Lys Cys
111 125 130 135
112 Leu Ser Glu Leu Ser Asn Leu Gln Glu Leu Tyr Ile Asn His Asn
113 140 145 150
114 Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe Ile Gly Leu His Asn
115 155 160 165
116 Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu Gln Met Ile Asn

```

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117		170		175		180									
118	Ser	Lys	Trp	Phe	Asp	Ala	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	Ile
119					185					190					195
120	Gly	Glu	Asn	Pro	Ile	Ile	Arg	Ile	Lys	Asp	Met	Asn	Phe	Lys	Pro
121					200					205					210
122	Leu	Ile	Asn	Leu	Arg	Ser	Leu	Val	Ile	Ala	Gly	Ile	Asn	Leu	Thr
123					215					220					225
124	Glu	Ile	Pro	Asp	Asn	Ala	Leu	Val	Gly	Leu	Glu	Asn	Leu	Glu	Ser
125					230					235					240
126	Ile	Ser	Phe	Tyr	Asp	Asn	Arg	Leu	Ile	Lys	Val	Pro	His	Val	Ala
127					245					250					255
128	Leu	Gln	Lys	Val	Val	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn
129					260					265					270
130	Pro	Ile	Asn	Arg	Ile	Arg	Arg	Gly	Asp	Phe	Ser	Asn	Met	Leu	His
131					275					280					285
132	Leu	Lys	Glu	Leu	Gly	Ile	Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile
133					290					295					300
134	Asp	Ser	Leu	Ala	Val	Asp	Asn	Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu
135					305					310					315
136	Ala	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Tyr	Ile	His	Pro	Asn	Ala	Phe
137					320					325					330
138	Phe	Arg	Leu	Pro	Lys	Leu	Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala
139					335					340					345
140	Leu	Ser	Ala	Leu	Tyr	His	Gly	Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu
141					350					355					360
142	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn	Pro	Ile	Arg	Cys	Asp	Cys	Val
143					365					370					375
144	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr	Asn	Ile	Arg	Phe	Met	Glu
145					380					385					390
146	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro	Glu	Phe	Gln	Gly	Gln
147					395					400					405
148	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met	Glu	Ile	Cys	Leu
149					410					415					420
150	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu	Asn	Val	Glu
151					425					430					435
152	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala	Glu	Pro
153					440					445					450
154	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu	Leu
155					455					460					465
156	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
157					470					475					480
158	Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr
159					485					490					495
160	Cys	Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met
161					500					505					510
162	Ile	Lys	Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu
163					515					520					525
164	Asn	Ile	Lys	Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser
165					530					535					540

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```

166 Trp Lys Ala Ser Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr
167                               545                               550
168 Ala Phe Val Lys Thr Glu Asn Ser His Ala Ala Gln Ser Ala Arg
169                               560                               565
170 Ile Pro Ser Asp Val Lys Val Tyr Asn Leu Thr His Leu Asn Pro
171                               575                               580
172 Ser Thr Glu Tyr Lys Ile Cys Ile Asp Ile Pro Thr Ile Tyr Gln
173                               590                               595
174 Lys Asn Arg Lys Lys Cys Val Asn Val Thr Thr Lys Gly Leu His
175                               605                               610
176 Pro Asp Gln Lys Glu Tyr Glu Lys Asn Asn Thr Thr Thr Leu Met
177                               620                               625
178 Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile Gly Val Ile Cys Leu
179                               635                               640
180 Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp Gly Gly His Ser
181                               650                               655
182 Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala Leu Gly Glu
183                               665                               670
184 Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys Glu Lys
185                               680                               685
186 Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro Thr
187                               695                               700

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188 Asn Met Ser

193 <210> SEQ ID NO: 3

194 <211> LENGTH: 1643

195 <212> TYPE: DNA

196 <213> ORGANISM: Homo sapiens

W--> 198 <220> FEATURE: -

199 <223> OTHER INFORMATION: 2635136

201 <400> SEQUENCE: 3

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202 tgcaatggcc atatgctgca gacccggagt gggtagttag ttggttaatg ccagtcttcc 60
203 tccccctggac actgagttct gctgacagcc cccgcccagc cagagctctg ctgtatacca 120
204 ccgggagtg ggctgggtgtg gagcctggag gtcgcccgt gccctcctag ggctgctcca 180
205 gacagcatta aaacgctgca ggctgcaggt gagactaaca gctgggagag ctgctccagg 240
206 catttaggac cctgactggg gcagatgagt cagcccagtg ggggcagggc tcctggaacg 300
207 aggatctaca gttggagttg cccactgtc atgtcacctg gagaaaaact ggaccaatt 360
208 cctgacagct tcattctgca accaccagtc ttccaccgg tggttcctta tgtcacgacg 420
209 atttttggag gcctgcatgc aggcaagatg gtcatgctgc aaggagtggg ccctctagat 480
210 gcacacaggt ttcaggtgga ctccagtggt ggctgcagcc tgtgtccccg gccagatata 540
211 gccttcact tcaaccctcg ctccataacc accaagcccc atgtcatctg caacaccctg 600
212 catgggtggac gctgggcaaag ggaggcccgg tggcccacc tggccctgag aagaggctcc 660
213 agcttctctca tcctctttct ctccgggaat gaggaagtga aggtgagtgat gaatggacag 720
214 cactttctcc acttcgcta ccggctccca ctgtctcatg tggacacgct ggtatatatt 780
215 ggtgacatcc tggtagaggc tgttggattc ctgaacatca atccatttgt ggagggcagc 840
216 agagagtacc cagctggaca tcctttctct ctgatgagcc ccaggctgga ggtgccctgc 900
217 tcacatgctc tccccaggg tctctcgct gggcaggtca tcatagtacg gggactggtc 960
218 ttgcaagagc cgaagcattt tactgtgagc ctgagggacc aggctgcccc tgctcctgtg 1020
219 acaactcagg cctccttcgc agacagaact ctggcctgga tctcccgtg ggggcagaag 1080
220 aaactgatct cagccccctt cctcttttac cccagagat tctttgaggt gctgctcctg 1140

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```

221 ttccaggagg gagggctgaa gctggcgctc aatgggcagg ggctgggggc caccagcatg 1200
222 aaccagcagg ccctggagca gctgcgggag ctccggatca gtggaagtgt ccagctctac 1260
223 tgtgtccact cctgaggatg gttccaggga aataccgcca gaaaacaaga aggtcagccc 1320
224 actoccaggg cccactctct cccccctcat taaaccatcc acctgacacc agcacatcag 1380
225 gcctggttca cctctggggt cactgagactg agtctacagg agctttgggc ctgagggaag 1440
226 gcacaagagt gcaaagggtc ctggaactct gcaccttctt ccaccaggag cctgggatat 1500
227 ggctccatct gccttcaggg cctggactgc actcacagag gcaagtgttg tagactaaca 1560
228 aagatactcc aaaatacaat ggcttaaaga atgtggtcat ttattcttta ttatttattt 1620
229 atttgtggtc aaataaataa ata                                     1643

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232 <210> SEQ ID NO: 4

233 <211> LENGTH: 2290

234 <212> TYPE: DNA

235 <213> ORGANISM: Homo sapiens

W--> 237 <220> FEATURE: -

238 <223> OTHER INFORMATION: 2687731

240 <400> SEQUENCE: 4

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241 cttactagca ctgactgtgg aatccttaag ggcccattac atttctgaag aagaaagcta 60
242 agatgaagga catgccactc cgaattcatg tgctacttgg cctagctatc actacactag 120
243 tacaagctgt agataaaaaa gtggattgtc cactggtatg tactgtgtaa atcaggcctt 180
244 ggtttacacc cagatccatt tatatggaag catctacagt ggattgtaat gatttaggtc 240
245 ttttaacttt cccagccaga ttgccagcta acacacagat tcttctccta cagactaaca 300
246 atattgcaaa aattgaatac tccacagact ttccagtaaa ccttactggc ctggatttat 360
247 ctcaaaaaca tttatcttca gtcaccaata ttaatgtaaa aaagatgcct cagctccttt 420
248 ctgtgtacct agaggaaaac aaacttactg aactgcctga aaaatgtctg tccgaactga 480
249 gcaacttaca agaactctat attaatcaca acttgccttc tacaatttca cctggagcct 540
250 ttattggcct acataatctt cttcgacttc atctcaattc aaatagattg cagatgatca 600
251 acagtaagtg gtttgatgct cttccaaatc tagagattct gatgattggg gaaaatccaa 660
252 ttatcagaat caaagacatg aactttaagc ctcttatcaa tcttcgcagc ctggttatag 720
253 ctggtataaa cctcacagaa ataccagata acgccttggg tggactggaa aacttagaaa 780
254 gcactctctt ttacgataac aggcttatta aagtacccca tgtgtctctt caaaaagttg 840
255 taaatctcaa atttttggat ctaaaataaa atcctattaa tagaatacga aggggtgatt 900
256 ttagcaatat gctacactta aaagagttgg ggataaataa tatgcctgag ctgatttcca 960
257 tcgatagtct tgctgtggat aacctgccag atttaagaaa aatagaagct actaacaacc 1020
258 ctagattgtc ttacattcac cccaatgcat ttttcagact cccaagctg gaatcactca 1080
259 tgetgaacag caatgctctc agtgccctgt accatggtag cattgagtct ctgcccacc 1140
260 tcaaggaaat cagcatacac agtaacccca tcagggtgtg ctgtgtcctc cgttggatga 1200
261 acatgaacaa aaccaacatt cgattcatgg agccagattc actgttttgc gtggaccac 1260
262 ctgaattcca aggtcagaat gttcggaag tgcatttcag ggacatgatg gaaatttgc 1320
263 tccctcttat agctcctgag agctttcctt ctaatctaaa ttagaagct gggagctatg 1380
264 tttcctttca ctgtagagct actgcagaac cacagcctga aatctactgg ataacacctt 1440
265 ctggtcaaaa actcttgctt aataccctga cagacaagtt ctatgtccat tctgagggaa 1500
266 cactagatat aaatggcgta actcccaaag aagggggttt atatacttgt atagcaacta 1560
267 acctagttag cgctgacttg aagtctgtta tgatcaaatg gtaggatctt ttccacaag 1620
268 ataacaatgg ctctttgaat attaaaataa gagatattca ggccaattca gttttggtgt 1680
269 cctggaaaagc aagttctaaa attctcaaat ctagtgttaa atggacagcc tttgtcaaga 1740
270 ctgaaaattc tcatgtgcg caaagtgtc gaataccatc tgatgtcaag gtatataatc 1800
271 ttactcatct gaatccatca actgagtata aaatttgtat tgatattccc accatctatc 1860
272 agaaaaacag aaaaaaatgt gtaaatgtca ccaccaaagg tttgcaccct gatcaaaaag 1920
273 agtatgaaaa gaataatacc acaacactta tggcctgtct tggaggcctt ctggggatta 1980

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VERIFICATION SUMMARY

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Input Set : A:\09747804.txt

Output Set: N:\CRF3\03222001\I747804.raw

L:31 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:90 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:198 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:237 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:287 M:256 W: Invalid Numeric Header Field, <220> has non-blank data